



SEQUENCE LISTING

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<150> PCT/US96/17957

<151> 1996-10-25

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Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser
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Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu
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Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala
90 95 100 105

cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga 509
Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro Ala Pro Gly

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	cca gaa gaa aca gtc act caa gac tgc ttg caa ctg att gca gac agt Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser			605
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	155	160	165	
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	cat gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt cga tgt att His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile			845
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	att gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca ata cca aga Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg			941
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Asp	Cys	Leu	Gln	Leu	Ile	Ala	Asp	Ser	Glu	Thr	Pro	Thr	Ile	Gln	Lys															
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Ala	Leu	Glu	Glu	Lys	Glu	Asn	Lys	Ile	Leu	Val	Lys	Glu	Thr	Gly	Tyr															
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Phe	Phe	Ile	Tyr	Gly	Gln	Val	Leu	Tyr	Thr	Asp	Lys	Thr	Tyr	Ala	Met															
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 Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
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Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
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His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
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Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
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Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro
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Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg
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 35 40 45
 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro
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 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
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 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
 85 90 95
 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
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 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
 115 120 125
 Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg
 130 135 140

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Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
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 Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
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 Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
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 Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
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 His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
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 Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
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tcaaagtcca agtagtgata tggatgactc cacagaaagg gagcagtcac gccttacttc 180
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 aggggaaaaat gcacaattat cactgggatg gagatgttca catttttttg gtgccattga 300
 aactgctgtg acctncttac ancangtgct gttingctatt ttncctncct nttctntggt 360
 aacctcttag gaaggaagga ttcttaactg ggaaataacc caaaaaaann ttaaangggg 420
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caaaggaaaa tctctactta gattnacaca tttgttccca tgggtntctt aagttttaa 360
aggggagtg ccttaggagg aaaaggggat aaatattggc caaggnaactg gttantttnt 420
aaatatgggc aggtttntat anctggtagg cctcgccatg ggcattnatt cangngagg 480
ncnntctttt gggntga 497
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<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer

<400> 10

gtgggatcca gcctccgggc agagctg 27

<210> 11

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer

<400> 11

gtgaagcttt tattacagca gtttcaatgc acc 33

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer

<400> 12

gtgtcatgag cctccgggca gagctg 26

<210> 13

<211> 33

B23

<212> DNA
 <213> Artificial Sequence
 <220>
 <221> primer_bind
 <223> primer
 <400> 13
 gtgaagcttt tattacagca gtttcaatgc acc 33

<210> 14
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> primer_bind
 <223> primer
 <400> 14
 gtgggatccc cgggcagagc tgcagggc 28

<210> 15
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> primer_bind
 <223> primer
 <400> 15
 gtgggatcct tattacagca gtttcaatgc acc 33

<210> 16
 <211> 129
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> primer_bind
 <223> primer
 <400> 16
 gcgggatccg ccaccatgaa ctctttctcc acaagcgct tcggtccagt tgccttctcc 60
 ctggggtgc tcctggtgtt gcctgctgcc ttccctgccc cagttgtgag acaaggggac 120
 ctggccagc 129

<210> 17
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> primer_bind
 <223> primer

B23

<400> 17
gtgggatcct tacagcagtt tcaatgcacc

30

<210> 18
<211> 903
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(798)

<400> 18
atg gat gac tcc aca gaa agg gag cag tca cgc ctt act tct tgc ctt 48
Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
1 5 10 15

aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca 96
Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
20 25 30

cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg 144
Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
35 40 45

gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg 192
Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
50 55 60

tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg 240
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
65 70 75 80

gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga 288
Ala Glu Leu Gln His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
85 90 95

gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg 336
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
100 105 110

aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac 384
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
115 120 125

agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gga tct tac 432
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr
130 135 140

aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa 480
Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu
145 150 155 160

gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata 528
Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile
165 170 175

tat ggt cag gtt tta tat act gat aag acc tac gcc atg gga cat cta 576

B23

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Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu
180                               185                               190

att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtg 624
Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val
195                               200                               205

act ttg ttt cga tgt att caa aat atg cct gaa aca cta ccc aat aat 672
Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn
210                               215                               220

tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga gat gaa ctc 720
Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu
225                               230                               235                               240

caa ctt gca ata cca aga gaa aat gca caa ata tca ctg gat gga gat 768
Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp
245                               250                               255

gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacctactt acaccatgtc 818
Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
260                               265

tgtagctatt ttcctccctt tctctgtacc tctaagaaga aagaatctaa ctgaaaatac 878

caaaaaaaaaa aaaaaaaaaa aaaaaa 903

```

<210> 19
 <211> 266
 <212> PRT
 <213> Homo sapiens

```

<400> 19
Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
1          5          10          15

Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
20          25          30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
35          40          45

Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
50          55          60

Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
65          70          75          80

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
85          90          95

Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
100         105         110

Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
115         120         125

Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr
130         135         140

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323

Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu
145 150 155 160

Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile
165 170 175

Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu
180 185 190

Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val
195 200 205

Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn
210 215 220

Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu
225 230 235 240

Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp
245 250 255

Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
260 265

<210> 20
<211> 136
<212> PRT
<213> Homo sapiens

<400> 20
His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp
1 5 10 15

Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg
20 25 30

Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val
35 40 45

Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met
50 55 60

Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe
65 70 75 80

Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
85 90 95

Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu Ser
100 105 110

Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly
115 120 125

Thr Phe Leu Gly Phe Val Lys Leu
130 135

B23

<210> 21
 <211> 462
 <212> DNA
 <213> Homo sapiens

<400> 21
 atggctgttc aggggtccgga agaaaccgtt actcaggact gccttcagct gatcgcagac 60
 tctgaaactc cgaccatcca gaaagggttct tacacctttg ttccttggct gctttctttc 120
 aaacgtgggt ctgccctgga agagaaagaa aacaaaatcc tggttaaaga aactgggttac 180
 ttctttatct acggtcaggt tctttacact gataagacct acgccatggg tcacctgatt 240
 cagcgtaaga aagttcacgt tttcgggtgac gagctgtctc tggttactct gtttcgctgc 300
 attcagaaca tgccggaac tcttcctaac aactcctgct actctgctgg catcgcaaaa 360
 ctggaagagg gtgatgaact gcagctggca attcctcgtg aaaacgcaca aatttctctg 420
 gacggtgatg taaccttctt tgggtgactg aaacttctgt aa 462

<210> 22
 <211> 1040
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(468)

<400> 22
 cgc gtg gta gac ctc tca gct cct cct gca cca tgc ctg cct gga tgc 48
 Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
 1 5 10 15
 cgc cat tct caa cat gat gat aat gga atg aac ctc aga aac aga act 96
 Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
 20 25 30
 tac aca ttt gtt cca tgg ctt ctc agc ttt aaa aga gga aat gcc ttg 144
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
 35 40 45
 gag gag aaa gag aac aaa ata gtg gtg agg caa aca ggc tat ttc ttc 192
 Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
 50 55 60
 atc tac agc cag gtt cta tac acg gac ccc atc ttt gct atg ggt cat 240
 Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
 65 70 75 80
 gtc atc cag agg aag aaa gta cac gtc ttt ggg gac gag ctg agc ctg 288
 Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 85 90 95
 gtg acc ctg ttc cga tgt att cag aat atg ccc aaa aca ctg ccc aac 336
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
 100 105 110
 aat tcc tgc tac tcg gct ggc atc gcg agg ctg gaa gaa gga gat gag 384
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
 115 120 125
 att cag ctt gca att cct cgg gag aat gca cag att tca cgc aac gga 432

B23

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Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
 130                      135                      140
gac gac acc ttc ttt ggt gcc cta aaa ctg ctg taa ctcacttgct      478
Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
145                      150                      155

ggagtgcgtg atcccccttcc ctcgtcttct ctgtacctcc gagggagaaa cagacgactg 538
gaaaaactaa aagatgggga aagccgtcag cgaaagtttt ctcgtgaccc gttgaatctg 598
atccaaacca ggaaatataa cagacagcca caaccgaagt gtgccatgtg agttatgaga 658
aacggagccc gcgctcagaa agaccggatg aggaagaccg ttttctccag tcctttgcca 718
acacgcaccg caaccttgct ttttgccttg ggtgacacat gttcagaatg cagggagatt 778
tccttggttt gcgatttgcc atgagaagag ggcccacaac tgcaggtcac tgaagcattc 838
acgctaagtc tcaggattta ctctcccttc tcatgctaag tacacacacg ctctttttcca 898
ggtaatacta tgggatacta tggaaagggt gtttggtttt aaatctagaa gtcttgaact 958
ggcaatagac aaaaatcctt ataaattcaa gtgtaaaata aacttaatta aaaaggttta 1018
agtggtgaaaa aaaaaaaaaa aa                                     1040

```

<210> 23
 <211> 155
 <212> PRT
 <213> Homo sapiens

```

<400> 23
Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
 1          5          10          15
Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
 20          25          30
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
 35          40          45
Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
 50          55          60
Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
 65          70          75          80
Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 85          90          95
Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
100          105          110
Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
115          120          125
Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
130          135          140
Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
145          150          155

```

<210> 24
 <211> 26
 <212> DNA
 <213> Artificial Sequence

B23

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<220>
<221> primer_bind
<223> primer

<400> 24
ccaccagctc caggagaagg caactc                                     26

<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 25
accgcgggac tgaaaaatct                                         19

<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 26
cacgcttatt tctgctgttc tga                                     23

<210> 27
<211> 657
<212> DNA
<213> Homo sapiens

<400> 27
taccaggtgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagggccac 60
cacgcggaga agctgccagc aagagcaaga gcccacaagg ccggtctggg ggaagctcca 120
gctgtcaccg caggactgaa aatctttgaa ccaccagctc caggagaagg caactccagt 180
cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcac tcaagactgc 240
ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttggt 300
ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taaaatattg 360
gtcaaagaaa ctgggttactt ttttatatat ggtcagggtt tatacactga taagacctat 420
gccatgggac atctaattca gaggaaaaaa gtccatgtct ttggggatga attgagtctg 480
gtgactttgt ttcgatgtat tcaaaatatg cctgaaacac tacccaataa ttctgctat 540
tcagctggca ttgcaaaact ggaagaagga gatgaacttc aacttgcaat accacgagaa 600
aatgcacaaa tatcactgga tggagatgtc acattttttg gtgccctcaa actgctg   657

<210> 28
<211> 219
<212> PRT
<213> Homo sapiens

<400> 28

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B23

Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
 1 5 10 15
 Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
 20 25 30
 Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
 35 40 45
 Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
 50 55 60
 Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
 65 70 75 80
 Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
 85 90 95
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
 100 105 110
 Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
 115 120 125
 Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
 130 135 140
 Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 145 150 155 160
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
 165 170 175
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
 180 185 190
 Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
 195 200 205
 Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 210 215

<210> 29

<211> 657

<212> DNA

<213> Homo sapiens

<400> 29

taccaggtgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagagccac 60
 cagcgggaga agctgccagc aagagcaaga gcccgaagg ccggtctggg ggaagctcca 120
 gctgtcaccg cgggactgaa aatctttgaa ccaccagctc caggagaagg caactccagt 180
 cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcac tcaagactgc 240
 ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttggt 300
 ccatggcttc tcagctttta aaggggaagt gccctagaag aaaaagagaa taaaatattg 360
 gtcaaagaaa ctggttactt ttttatatat ggtcagggtt tatacactga taagacctat 420
 gccatgggac atctaattca gaggaaaaaa gtccatgtct ttggggatga attgagctct 480
 gtgactttgt ttcgatgtat tcaaaatatg cctgaaacac taccataata ttcttgctat 540
 tcagctggca ttgcaaaact ggaagaagg gatgaacttc aacttgcaat accacgagaa 600
 aatgcacaaa tatcactgga tggagatgtc acattttttg gtgccctcaa actgctg 657

B23

<210> 30
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 30

Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
 1 5 10 15
 Leu Gln Ser His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
 20 25 30
 Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
 35 40 45
 Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
 50 55 60
 Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
 65 70 75 80
 Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
 85 90 95
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
 100 105 110
 Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
 115 120 125
 Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
 130 135 140
 Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 145 150 155 160
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
 165 170 175
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
 180 185 190
 Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
 195 200 205
 Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 210 215

<210> 31
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <223> primer

B23

<400> 31
ggtcgcccgtt tctaacgcgg ccgttcaggg tccagaag 38

<210> 32
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 32
ctgggttcggc ccaagggtacc aagcttgtagc cttagatctt ttctagatc 49

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 33
ctggtagttc ttcggagtg g 21

<210> 34
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 34
cgcgtagaa acggcgacc 19

<210> 35
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<220>
<221> misc_feature
<222> (7)
<223> n equals deoxyinosine

<220>
<221> misc_feature

B23

<222> (12)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (16)
<223> n equals deoxyinosine

<400> 35
taccagntgg cngccntgca ag

22

<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<220>
<221> misc_feature
<222> (3)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (14)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (16)..(17)
<223> n equals deoxyinosine

<400> 36
gtnacagcag tttnanngca cc

22

<210> 37
<211> 866
<212> DNA
<213> Mus musculus

<400> 37
atggatgagt ctgcaaagac cctgccacca ccgtgcctct gtttttgctc cgagaaagga 60
gaagatatga aagtgggata tgatcccac actccgcaga aggaggaggg tgccctgggtt 120
gggatctgca gggatggaag gctgctggct gctaccctcc tgctggccct gttgtccagc 180
agtttcacag cgatgtcctt gtaccagttg gctgccttgc aagcagacct gatgaacctg 240
cgcattggagc tgcagagcta ccgaggttca gcaacaccag ccgccgcggg tgctccagag 300
ttgaccgctg gagtcaaact cctgacaccg gcagctcctc gaccccacaa ctccagccgc 360
ggccacagga acagacgcgc cttccaggga ccagaggaaa cagaacaaga tgtagacctc 420
tcagctcctc ctgcaccatg cctgcctgga tgccgccatt ctcaacatga tgataatgga 480
atgaacctca gaaacatcat tcaagactgt ctgcagctga ttgcagacag cgacacgccg 540
gccttgaggg agaaagagaa caaaatagtg gtgaggcaaa caggctattt cttcatctac 600
agccagggtc tatacacgga ccccatcttt gctatgggtc atgtcatcca gaggaagaaa 660
gtacacgtct ttggggacga gctgagcctg gtgaccctgt tccgatgtat tcagaatatg 720
cccaaaacac tgcccaacaa ttcttgctac tcggctggca tcgagaggct ggaagaagga 780
gatgagattc agcttgcaat tcctcgggag aatgcacaga tttcacgcaa cggagacgac 840
accttctttg gtgcctctaa actgct 866

B23

<210> 38
 <211> 289
 <212> PRT
 <213> Mus musculus

<400> 38

Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys
 1 5 10 15

Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
 20 25 30

Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
 35 40 45

Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
 50 55 60

Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
 65 70 75 80

Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
 85 90 95

Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
 100 105 110

Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
 115 120 125

Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
 130 135 140

Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
 145 150 155 160

Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
 165 170 175

Ser Asp Thr Pro Ala Leu Glu Glu Lys Glu Asn Lys Ile Val Val Arg
 180 185 190

Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro
 195 200 205

Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His Val Phe
 210 215 220

Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met
 225 230 235 240

Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg
 245 250 255

Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala
 260 265 270

Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu

B23

275

280

285

Leu

<210> 39

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer

<400> 39

cagactggat ccgccacccat ggatgactcc acagaaag

38

<210> 40

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer

<400> 40

cagactggta ccgtcctgcg tgcactacat ggc

33

<210> 41

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<212> DNA

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